Claim 4. (Amended) A human SMN gene according to Claim 3, which comprises the following intronic sequences:

-for intron n° 6 SEQ ID NO:1:

[5' AATTTTTAAATTTTTTGTAGAGACAGGGTCTCATTATGTTGCCCAGGGTG
GTGTCAAGCTCCAGGTCTCAAGTGATCCCCCTACCTCCGCCTCCCAAAGTTGT
GGGATTGTAGGCATGAGCCACTGCAAGAAAACCTTAACTGCAGCCTAATAATT
GTTTTCTTTGGGATAACTTTTAAAGTACATTAAAAGACTATCAACTTAATTTC
TGATCATATTTTGTTGAATAAAATAAGTAAAATGTCTTGTGAACAAAATGCTT
TTTAACATCCATATAAAGCTATCTATATATAGCTATCTATGTCTATATAGCTA
TTTTTTTTAACTTCCTTTTATTTTCCTTACAG 3']

-for intron n° 7 SEQ ID NO:2:

[5' GTAAGTCTGCCAGCATTATGAAAGTGAATCTTACTTTTGTAAAACTTTAT
GGTTTGTGGAAAACAAATGTTTTTGAACAGTTAAAAAGTTCAGATGTTAAAAA
GTTGAAAGGTTAATGTAAAACAATCAATATTAAAGAATTTTGATGCCAAAACT
ATTAGATAAAAGGTTAATCTACATCCCTACTAGAATTCTCATACTTAACTGGT
TGGTTATGTGGAAGAAACATACTTTCACAATAAAGAGCTTTAGGATATGATGC
CATTTTATATCACTAGTAGGCAGACCAGCAGACTTTTTTTTATTGTGATATGG
GATAACCTAGGCATACTGCACTGTACACTCTGACATATGAAGTGCTCCTAGTCA
AGTTTAACTGGTGTCCACAGAGGACATGGTTTAACTGGAATTCGTCAAGCCTC
TGGTTCTAATTTCTCATTTGCAG 3'].

Claim 10, line 2, change "Claim 3" to --cDNA sequence of Fig. 3--;

change "in stringents" to --under stringent--;

line 3, change "Claims 1 to 9" to --Claims 3 to 9--.

Claim 14. (Amended) An isolated nucleotide sequence selected among the following sequences:

5' AGACTATCAACTTAATTTCTGATCA 3' (SEQ ID NO:5)

5' TAAGGAATGTGAGCACCTTCCTTC 3' (SEQ ID NO:6)

5' GTAATAACCAAATGCAATGTGAA 3' (SEQ ID NO:7)

5' CTACAACACCCTTCTCACAG 3' (SEQ ID NO:8)

Claim 15. (Amended) A set of primers comprising:

-a pair of primers contained in the sequence comprising nucleotides 921 to 1469 of the sequence of Figure 3 and/or

-a pair of primers comprising the following sequences:

5' AGACTATCAACTTAATTTCTGATCA 3' (SEQ ID NO:5)

5' TAAGGAATGTGAGCACCTTCCTTC 3' (SEQ ID NO:6).

Claim 16. (Amended) A set of primers selected from the group consisting of:

5' AGACTATCAACTTAATTTCTGATCA 3' (SEQ ID NO:5)

5' TAAGGAATGTGAGCACCTTCCTTC 3' (SEQ ID NO:6)

5' GTAATAACCAAATGCAATGTGAA 3' (SEQ ID NO:7)

5' CTACAACACCCTTCTCACAG 3' (SEQ ID NO:8)

5' AGG GCG AGG CTC TGT CTC A 3' (SEQ ID NO:24)

5' CGG GAG GAC CGC TTG TAG T 3' (SEQ ID NO:25);

5' GCC GGA AGT CGT CAC TCT T 3' (SEQ ID NO:26)

5' GGG TGC TGA GAG CGC TAA TA 3' (SEQ ID NO:27);

5' TGT GTG GAT TAA GAT GAC TC 3' (SEQ ID NO:28)

5' CAC TTT ATC GTA TGT TAT C 3' (SEQ ID NO:29);

5' CTG TGC ACC ACC CTG TAA CAT G 3' (SEQ ID NO:30)

5' AAG GAC TAA TGA GAC ATC C 3' (SEQ ID NO:31);

5' CGA GAT GAT AGT TTG CCC TC 3' (SEQ ID NO:32)

5' AG CTA CTT CAC AGA TTG GGG AAA G 3' (SEQ ID NO:33);

5' CTC ATC TAG TCT CTG CTT CC 3' (SEQ ID NO:34)

B3 cont.

5' TGG ATA TGG AAA TAG AGA GGG AGC 3' (SEQ ID NO:35);

5' CAC CCT TAT AAC AAA AAC CTG C 3' (SEQ ID NO:36)

5' GAG AAA GGA GTT CCA TGG AGC AG 3' (SEQ ID NO:37);

5' GAG AGG TTA AAT GTC CCG AC 3' (SEQ ID NO:38)

5' GTG AGA ACT CCA GGT CTC CTG G 3' (SEQ ID NO:39);

5' TGA GTC TGT TTG ACT TCA GG 3' (SEQ ID NO:40)

5' GAA GGA AAT GGA GGC AGC CAG C 3' (SEQ ID NO:41);

5' TTT CTA CCC ATT AGA ATC TGG 3' (SEQ ID NO:42)

5' CCC CAC TTA CTA TCA TGC TGG CTG 3' (SEQ ID NO:43);

5' CCA GAC TTT ACT TTT TGT TTA CTG 3' (SEQ ID NO:44)

5' ATA GCC ACT CAT GTA CCA TGA 3' (SEQ ID NO:45);

5' AAG AGT AAT TTA AGC CTC AGA CAG 3' (SEQ ID NO:46)

5' CTC CCA TAT GTC CAG ATT CTC TTG 3' (SEQ ID NO:47);

5' AGA CTA TCA ACT TAA TTT CTG ATC A 3' (SEQ ID NO:48)

5' TAA GGA ATG TGA GCA CCT TCC TTC 3' (SEQ ID NO:49);

5' AGA CTA TCA ACT TAA TTT CTG ATC A 3' (SEQ ID NO:50)

5' GTA AGA TTC ACT TTC ATA ATG CTG 3' (SEQ ID NO:51);

5' CTT TAT GGT TTG TGG AAA ACA 3' (SEQ ID NO:52)

5' GGC ATC ATA TCC TAA AGC TC 3' (SEQ ID NO:53);

[5' CGA GAT GAT AGT TTG CCC TC 3'

5' AG CTA CTT CAC AGA TTG GGG AAA G 3';

5' CTC ATC TAG TGT CTG CTT CC 3'

5' TGG ATA TGG AAA TAG AGA GGG AGC 3';

5' CAC CCT TAT AAC AAA AAC CTG C 3'

5' GAG AAA GGA GTT CCA TGG AGC AG 3';

5' GAG AGG TTA AAT GTC CCG AC 3'

5' GTG AGA ACT CCA GGT CTC CTG G 3';

5' TGA GTC TGT TTG ACT TCA GG 3'

5' GAA GGA AAT GGA GGC AGC CAG C 3';

5' TTT CTA CCC ATT AGA ATC TGG 3'

5' CCC CAC TTA CTA TCA TGC TGG CTG 3';

5' CCA GAC TTT ACT TTT TGT TTA CTG 3'

5' ATA GCC ACT CAT GTA CCA TGA 3';

5' AAG AGT AAT TTA AGC CTC AGA CAG 3'

5' CTC CCA TAT GTC CAG ATT CTC TTG 3';

5' AGA CTA TCA ACT TAA TTT CTG ATC A 3'

5' TAA GGA ATG TGA GCA CCT TCC TTC 3';

5' AGA CTA TCA ACT TAA TTT CTG ATC A 3'

5' GTA AGA TTC ACT TTC ATA ATG CTG 3';

5' CTT TAT GGT TTG TGG AAA ACA 3'

5' GGC ATC ATA TCC TAA AGC TC 3';]

5' GTA ATA ACC AAA TGC AAT GTG AA 3' (SEQ ID NO:54)

5' CTA CAA CAC CCT TCT CAC AG 3' (SEQ ID NO:55); and

5' GGT GTC CAC AGA GGA CAT GG 3' (SEQ ID NO:56)

5' AAG AGT TAA CCC ATT CCA GCT TCC 3' (SEQ ID NO:57).

B3 Cont.

Claim 17, line 2, change "Claims 1 to 11" to --Claims 3 to 9 and 11--.

Claim 23, line 1, delete "21 or"

Claim 24, line 2, change "Claims 1 to 11" to --Claims 3 to 9 and 11--.

Claim 28, lines 2-3, change "any one of Claims 24 to 27" to --Claim 24--.

Claim 29, line 2, change "Claims 1 to 11" to --Claims 3 to 9 and 11--.

Please add the following new claims:

--31. The method of Claim 30, wherein said motor neuron disorder is spinal muscular atrophy.--

--32. The method of Claim 30, wherein steps (c) and (d) are replaced with a step of digestion with a Bsrl enzyme.--

--33. A method for detecting spinal muscular atrophy said method comprising the steps of:

(a) extracting DNA from a patient sample;

(b) hybridizing said DNA with a DNA probe comprising all or part of the DNA sequence of Figure 3 under stringent conditions; and

(c) detecting the hybrids possibly formed.--

--34. The method according to Claim 33, wherein said probe is radiolabeled.--

--35. A monoclonal antibody or a polyclonal antiserum directed against the SMN protein of Figure 1, or against the protein of Figure 8, or against the protein of Figure 12.--

--36. A method for detecting arthrogryposis multiplex congenita (AMC), said method comprising the steps of:

(a) extracting DNA from a patient sample;

(b) amplifying said DNA via PCR using unlabeled primers from exon 7 and exon 8 of the SMN gene;

(c) subjecting said amplified DNA to SCCP;

(d) autoradiographing the gels; and

(e) detecting the presence or absence of arthrogryposis multiplex congenita.--

--37. An isolated nucleotide sequence of Figure 11.--

--38. A transgenic mouse that only expresses the human SMN protein of Figure 1.--

--39. A transgenic mouse that expresses a mutated SMN protein of Figure 1.--

--40. A method of detecting the presence in a human patient of an altered SMN gene associated with spinal muscular atrophy, comprising

analyzing exon 7 or exon 8 of a gene identified as T-BCD541 in a biological sample derived from the patient, and

comparing said exon to the corresponding exon derived from T-BCD541 from normal human tissue;

wherein an alteration of either exon 7 or exon 8 in said patient sample with reference to said normal tissue is indicative of the presence of an altered SMN gene associated with spinal muscular atrophy in said patient.--

--41. The method of claim 40, wherein said analyzing comprises

determining whether T-BCD541 exon 7 is present or absent in the patient sample.--

--42. The method of claim 40, wherein said analyzing comprises

determining whether T-BCD541 exon 8 is present or absent in the patient sample.--

--43. The method of either of claim 40, wherein said analyzing includes amplifying all or part of the T-BCD541 gene.--

--44. The method of claim 43, wherein said analyzing comprises

amplifying a nucleotide fragment from said patient sample comprising exon 7 of the T-BCD541 gene,

amplifying a nucleotide fragment from said patient sample comprising exon 8 of the T-BCD541 gene, and

determining whether said exon 7 and said exon 8 are present or absent in said amplified fragments.--

--45. The method of claim 44, wherein said determining includes

subjecting said exon 7 comprising nucleotide fragment to restriction enzyme digestion,

subjecting said exon 8 comprising nucleotide fragment to restriction enzyme digestion, and

analyzing enzymatic digestion products produced by said enzymatic digestions,

wherein an alteration of either exon 7 or exon 8 with reference to normal tissue is evidenced by an altered restriction enzymatic digestion pattern in one or both of said exons.--

--46. The method of claim 43, wherein said amplifying is carried out using a polymerase chain reaction using a primer

selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8.--

--47. The method of claim 40, wherein said analyzing comprises subjecting said patient T-BCD541 gene to restriction cleavage.--

--48. The method of claim 40, wherein said analyzing comprises subjecting said patient T-BCD541 gene to single strand conformation polymorphism analysis.

--49. The method of claim 40, wherein said biological sample is selected from the group consisting of blood, cerebral fluid, peripheral blood leukocytes, a lymphoblastoid cell line and muscle tissue.--

--50. A method of confirming a clinical diagnosis of arthrogryposis multiplex congenita in a patient, comprising

analyzing exon 7 or exon 8 of a gene identified as T-BCD541 in a biological sample derived from the patient, and

comparing said exon to the corresponding exon derived from T-BCD541 from normal human tissue;

wherein an alteration of either exon 7 or exon 8 in said patient sample with reference to said normal tissue is indicative of the presence of an altered SMN gene associated with arthrogryposis multiplex congenita in said patient.--

--51. The method of claim 50, wherein said analyzing comprises

amplifying a nucleotide fragment from said patient sample comprising exon 7 of the T-BCD541 gene,

amplifying a nucleotide fragment of said patient sample comprising exon 8 of the T-BCD541 gene, and

determining whether said exon 7 and said exon 8 are present or absent in said amplified nucleotide fragments.--

--52. The method of claim 51, wherein said determining includes

subjecting said exon 7 comprising nucleotide fragment to restriction enzyme digestion,

subjecting said exon 8 comprising nucleotide fragment to restriction enzyme digestion, and

analyzing enzymatic digestion products produced by said enzymatic digestions,

wherein an alteration of either exon 7 or exon 8 with reference to normal tissue is evidenced by an altered restriction enzymatic digestion pattern in one or both of said exons.--

REMARKS

Enclosed herewith in full compliance with 37 C.F.R. §1.821-1.825 is a Substitute Sequence Listing to be inserted into the